# Max Homilius

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mxhm.github.io

## Professional experience

**since 09/2024**

Senior Data Scientist
Office of Data Sciences
Nationwide Children's Hospital

Analysis of **pediatric genetic conditions** using curated phenotypes and those extracted from medical notes. Identification of **novel gene-phenotype associations** in pediatric populations. Development of **natural language-based systems** for clinicians and researchers to use phenotypic and genetic queries, bridging genomic data and clinical applications.

**04/2019-09/2024**

Postdoctoral Research Fellow
Brigham and Women's Hospital
Harvard Medical School

Development of **machine learning algorithms** for the analysis of biomedical data from modalities such as blood cytometry, electrocardiogram recordings, medical notes and wearable device sensors. **Genetic association studies** using novel phenotypes, such as blood cell perturbation responses and deep learning-derived cardiac traits in biobank-scale cohorts. Integrative analyses of **sequencing, metabolomic and proteomic data** in human and animal models, including metagenomic analyses of gut microbiome data.

**09/2018-02/2019**

Postdoctoral Research Associate
Troyanskaya Laboratory
Lewis-Sigler Institute for Integrative Genomics
Princeton University

## Education

**2018**  PhD Computer Science, Princeton University
Thesis: "Network-Based Prioritization of Disease Genes, Animal Models, and Drug Targets"
Adviser: Dr. Olga Troyanskaya

**2014**  MA Computer Science, Princeton University

**2011**  MPhil Computational Biology, University of Cambridge
Thesis: "Bootstrap Aggregating for Phylogenetic Inference"
Adviser: Dr. Florian Markowetz

**2009**  BSc Bioinformatics, Free University of Berlin
Thesis: "Supertree Heuristics on Reduced Sets of Triplets"
Adviser: Dr. Oliver Eulenstein

## Publications and presentations

### Articles

**Homilius M\***, Zhu W\*, Eddy S, Thompson P, Zheng H, Xuan L, Kim D, Nsubuga C, Strecker Z, Cho J, Evans C, Howie M, Thaler AA, Wilson E, Gupta P, Cupelo M, Smith C, Nascimben J, Sridaran S, Lunati G, Folks H, Rheinstein C, Pettit C, Ghosal A, Truslow J, Wollison B, Goto S, Warren C, Vandenwijngaert S, MacRae CA and Deo RC. "Perturbational phenotyping of human blood cells reveals genetically determined latent traits associated with

subsets of common diseases". *Nat Genet* 10.1038/s41588-023-01600-x, 2023.

Kailas P*, **Homilius M**\*, Deo RC, MacRae CA. "Contrastive Language-Diagnostic Pretraining for automated adjudication of medical notes". Machine Learning for Health, Proceedings of Machine Learning Research 225:201–216, 2023.

Kailas P*, **Homilius M**\*, Goto S*, Nascimben J, Smith C, Cupelo M, MacRae CA, Deo RC. "Robust de-identification of medical notes using transformer architectures, sentence context and recall thresholding". Submitted.

Goto S, Solanki D, John JE, Yagi R, **Homilius M**, Ichihara G, Katsumata Y, Gaggin HK, Itabashi Y, MacRae CA and Deo RC. "Multinational Federated Learning Approach to Train ECG and Echocardiogram Models for Hypertrophic Cardiomyopathy Detection.", *Circulation* 146(10), 755-769, 2022.

Truslow JG, Goto S, **Homilius M**, Mow C, Higgins JM, MacRae CA, Deo RC. "Cardiovascular Risk Assessment Using Artificial Intelligence-Enabled Event Adjudication and Hematologic Predictors.", *Circ Cardiovasc Qual Outcomes* 15(6):e008007, 2022.

Zhu W, Guo S, **Homilius M**, Nsubuga C, Wright SH, Quan D, Kc A, Eddy SS, Victorio RA, Beerens M, Flaumenhaft R, Deo RC, MacRae CA. "PIEZO1 mediates a mechanothrombotic pathway in diabetes.", *Sci Transl Med* 14(626):p.eabk1707, 2022.

Goto S, Werdich AA, **Homilius M**, John JE, Gan L, MacRae CA, DiCarli MF, Deo RC. "Discovery of cardiac imaging biomarkers by training neural network models across diagnostic modalities". Preprint [medRxiv:2021.02.07.21251025], 2021.

Goto S*, **Homilius M\***, John JE, Truslow JG, Werdich AA, Blood AJ, Park BH, MacRae CA, Deo RC. "Artificial intelligence-enabled event adjudication: estimating delayed cardiovascular effects of respiratory viruses". Preprint [medRxiv:2020.11.12.20230706], 2020.

Goya J, Wong AK, Yao V, Krishnan A, **Homilius M**, Troyanskaya OG. "FNTM: a server for predicting functional networks of tissues in mouse.", *Nucleic Acids Research* 43 (W1): W182-W187, 2015.

Bansal M, …, **NCI-DREAM Community**. "A Community computational challenge to predict the activity of pairs of compounds.", *Nature Biotechnology* 32, 1213–1222, 2014.

Yosef N, Zalckvar E, Rubinstein A, **Homilius M**, Atias N, Vardi L, Berman I, Zur H, Kimchi A, Ruppin E, Sharan R "ANAT: a tool for constructing and analyzing functional protein networks." *Science Signaling* 196, pl1, 2011.

**Homilius M**, Wiedenhoeft J, Thieme S, Standfuß C, Kel I, Krause R. "Cocos: Constructing multi-domain protein phylogenies." *PLoS Currents* 3:RRN1240, 2011.

**Manuscripts in preparation**

Saha K, **Homilius M**, MacRae CA. "Hypoxia pathway contributes to cyanide resistance in developing zebrafish embryos".

Yagi R, **Homilius M**\*, Katsumata Y, MacRae CA, Goto S, Deo RC. "Using artificial intelligence to identify key electrocardiographic features for detecting left ventricular systolic dysfunction".

**Conference proceedings and posters**

2019    **Homilius M**, Blood AJ, Park BH, Yazdi D, Veytsman JN, MacRae CA, Deo RC. "Automated Disease Detection Using Document Classification Outperforms Encounter-Level Diagnostic Codes for Cardiovascular Diseases", American Heart Association Scientific Sessions, Philadelphia, Nov 16-18, 2019.

2018    **Homilius M**, Ricciotti E, Krishnan A, MacRae C, Grosser T, FitzGerald G, Troyanskaya O. "Prioritizing animal models and drug targets using functional networks", CIFAR Genetic Networks Program Meeting, Toronto, June 02, 2018.

2016    **Homilius M**, Ricciotti E, Krishnan A, Grosser T, Troyanskaya O. "A network-based approach to detect drug mode-of-action at therapeutic doses", New York Area meeting on Computational and Statistical Genomics, Cold Spring Harbor Laboratory, July 20, 2016.

2015    **Homilius M**, Krishnan A, MacRae C, Troyanskaya O. "Prioritizing animal models for human diseases using genome-wide functional networks", RECOMB/ISCB Conference on Regulatory

and Systems Genomics, Philadelphia, Nov 15-18, 2015.

2010   **Homilius M**, Burleigh G, Eulenstein O. "Triplet-supertrees constructed from minimum triplet presentations", BICoB 2010, 127-132.

## Teaching

9/2012-1/2013   Assistant in Instruction, Integrated Science Curriculum (General Computer Science I) Princeton University

2/2013-6/2013   Assistant in Instruction, Integrated Science Curriculum (General Computer Science II) Princeton University

## Previous research positions

3/2010-9/2010   *Research assistant*, Max Planck Institute of Molecular Genetics
Dr. Martin Vingron and Dr. Roland Krause, Research Advisers
Design and implementation of a program for the inference of the joint phylogeny of multi-domain proteins.

11/2008-12/2008   *Undergraduate researcher*, Max Planck Institute of Molecular Genetics
Dr. Hans Lehrach and Dr. Lukas Chavez, Research Advisers
Statistical analysis of DNA methylation data.

08/2008-10/2008   *Undergraduate researcher*, Tel Aviv University
Dr. Roded Sharan and Dr. Nir Yosef, Research Advisers
Implementation of a program for the generation, analysis and refinement of functional sub-networks in protein interaction networks.

## Honors and awards

2022-2023   Drs. Tobia and Morton Mower Fellow
2010-2011   German Academic Scholarship Foundation Study Abroad Stipend (University of Cambridge)
2008-2011   German Academic Scholarship Foundation Fellow
2008   German Academic Exchange Service Travel Award (Tel Aviv University)

## Service

2018-2023   Peer review, *Journal of Computational Biology*
2020   Peer review, *Pacific Symposium on Biocomputing*
2016   Peer review, *RECOMB/ISCB Conference on Regulatory and Systems Genomics*
2015, 2018   Peer review, *Circulation: Cardiovascular Genetics*